What is claimed is:

1. A nucleic acid probe array comprising a set of probes for interrogating the joining sequence between a first sequence element and a second sequence element.

2. The probe array of Claim 1 wherein said nucleic acid is oligonucleotide.

3. The probe array of Claim 1 wherein said first sequence element is a first exon and said second sequence element is a second exon.

4. The probe array of Claim 3 wherein said joining sequence is the 3' sequence of said first exon and 5' sequence of said second exon.

5. The probe array of Claim 4 wherein said joining sequence is at least 20 bases.

6. The probe array of Claim 5 wherein said joining sequence is at least 30 bases.

7. The probe array of Claim 6 wherein said joining sequence is at least 40 bases.

8. The probe array of Claim 7 wherein said joining sequence is at least 50 bases.

9. The probe array of Claim 8 wherein said joining sequence is at least 100 bases.

10. The probe array of Claim 1 wherein said set of probes are immobilized on a substrate at a density of at least 100 probes/cm^2.

11. A method for determining target sequence wherein said target sequence comprises a first sequence element joining a second sequence element comprising:

a) hybridizing said target sequence with a nucleic acid probe array comprising a set of probes for interrogating the joining sequence between said first sequence element and said second sequence element; and

b) obtaining information about the joining sequence based upon the

hybridization of said target sequence with said set of probes.

12. The method of Claim 11 wherein said first and second sequence elements are exons.

13. The method of Claim 12 wherein said set of nucleic acid probes are oligonucleotide probes.

14. The method of Claim 13 wherein said set of nucleic acid probes are immobilized on a substrate.

15. The method of Claim 14 wherein said set of nucleic acid probes are immobilized at a density of at least 100 probes/cm^2.

16. The method of Claim 12 wherein said target sequence is a mRNA.

17. The method of Claim 16 wherein said mRNA is one of at least two alternatively spliced mRNAs transcribed from a gene.

18. The method of Claim 11 further comprising the step of quantifying said first and second sequence elements using said information about the joining sequence and said hybridization.

19. The method of Claim 11 wherein said nucleic acid probe array comprising sequence probes against said first and second sequence elements.

20. The method of Claim 19 further comprising quantifying said first and second sequence elements based upon the hybridization of said target sequence and said sequence probes.

21. The method of Claim 11 wherein said probes for interrogating are probes for tiling said joining sequence.

22. The method of Claim 21 wherein said joining sequence is at least 20 bases.

23. The method of Claim 22 wherein said joining sequence is at least 30 bases.

24. The method of Claim 23 wherein said joining sequence is at least 40 bases.

25. The method of Claim 24 wherein said joining sequence is at least 50 bases.

26. The method of Claim 25 wherein said joining sequence is at least 100 bases.

27. The method of Claim 19 wherein said probes are oligonucleotides.

28. A computer software product comprising:

a) Computer code that receives a plurality of hybridization signals, wherein each of said plurality of signals reflects the hybridization of one of plurality of tiling probes to interrogate the joining sequence of a target sequence wherein said target sequence has at least one sequence element that is selected from a group of at least two sequence elements;

b) Computer code that identifies said sequence element based upon said hybridization signals; and

c) A computer readable media that stores said codes.

29. The computer software of Claim 28 wherein said tiling probes are oligonucleotides immobilized on a substrate.

30. The computer software of Claim 29 wherein said tiling probes interrogate at least 20 bases.

31. The computer software of Claim 29 wherein said tiling probes interrogate at least 30 bases.

32. The computer software of Claim 29 wherein said tiling probes interrogate at least 40 bases.

33. The computer software of Claim 29 wherein said tiling probes interrogate at

least 50 bases.

34. The computer software of Claim 29 wherein said tiling probes interrogate at least 100 bases.

35. The computer software of Claim 28 further comprising computer code that quantifies said target sequence.

36. A method for designing probes for detecting the combination of two sequence elements comprising:

a) inputting the sequence of the joining region between said two sequence elements; and

b) selecting probes for tiling the said joining region based upon said sequence.

37. The method of Claim 36 wherein said two sequence elements are exons.

38. The method of Claim 37 further comprising a step of designing lithographic mask wherein said lithographic mask is used in the fabrication of arrays of nucleic acid probes.

39. The method of Claim 38 further comprising a step of output signals for controlling an ink-jet printing mechanism for depositing compounds on a substrate.

40. The method of Claim 38 wherein said sequence is at least 20 bases.

41. The method of Claim 40 wherein said sequence is at least 30 bases.

42. The method of Claim 41 wherein said sequence is at least 40 bases.

43. The method of Claim 42 wherein said sequence is at least 50 bases.

44. The method of Claim 43 wherein said sequence is at least 100 bases.

45. A computer software product comprising:

a) a computer program code that constructs a joining sequence;

b) a computer program code that selects tiling probes to interrogate said joining sequence; and

c) a computer readable media that stores said codes.

46. The computer software product of Claim 45 wherein said joining sequence is for one of alternatively spliced mRNAs.

47. The computer software product of Claim 46 further comprising computer code that inputs exon sequences of one gene.

48. The computer software product of Claim 47 wherein said joining sequence is constructed based upon said exon sequences.

49. The computer software product of Claim 48 further comprising code that outputs sequence of said probes.